

Sequence Listing

<11> Genbank, Inc. and Curran Corporation

<12> NUCLEIC ACID SEQUENCES, THEIR ANALYSIS, AND METHODS FOR THEIR USE IN AMPLIFICATION AND VARIATION

<13> 11/19/84/PT

<14> 2/15-15-85

<15> US 60/159,587

<151> 1999-10-57

<152> US 60/162,611

<153> 1999-10-28

<160> 29

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<212> DNA

<213> Homo sapiens

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gcc gcc aag gtg ctg ctg gac gac aag gtg ccg ctg aca 128
Ala Gly Lys Val Leu Leu Asp Asp Thr Val Pro Leu Thr
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gca gcc atc gag ggc agc cag agc ctg cag tcc cac aag 167
Ala Ala Ile Glu Ala Ser Gln Ser Leu Gln Ser His Thr
25 30

gaa tat att att cga gtg caa aga gga att tct gtg gaa 206
Glu Tyr Ile Ile Arg Val Gln Arg Gly Ile Ser Val Glu
35 40 45

aac agc tgg cag att gtt aga aga tac agt gac ttt gat 245
Asn Ser Trp Gln Ile Val Arg Arg Tyr Ser Asp Phe Asp
50 55 60

ttg ctt aac aac agc tta cag att gca gcc cta agt cta 284
Leu Leu Asn Asn Ser Leu Gln Ile Ala Gly Leu Ser Leu
65 70

cat ctt cat ccc aac aac tta att ggt aac atg gat cgt 323
Pro Leu Pro Pro Lys Lys Leu Ile Gly Asn Met Asp Arg
75 80 85

gaa ttc ata cat gaa agc cag aac att ctt cag aac tat 362
Glu Phe Ile Ala Gln Arg Gln Lys Gly Leu Gln Asn Tyr
90 95

ctc aac gtg atc aca aca aat cat atc ttg tct aat tgt 401
Leu Asn Val Ile Thr Thr Asn His Ile Leu Ser Asn Cys
100 105 110

111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 44
 Val Leu Val Lys Lys Ile Leu Asp Ile Asn Asn Tyr Ser
 11 121 121

5 111 111 111 111 111 111 111 111 111 111 111 111 111 111 474
 Ala Asn Tyr Thr Gln Ile Ala Leu Gln Gln Val Ser Met
 11 121

10 111 111 111 111 111 111 111 111 111 111 111 111 111 111 514
 Ile Ile Arg Ser Ala Pro Lys Trp Ala Val Val Ile Pro
 140 145 150

15 111 111 111 111 111 111 111 111 111 111 111 111 111 111 557
 Leu Lys Asp Ile Gly Trp Arg Ile Arg Lys Lys Tyr Phe
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20 111 111 111 111 111 111 111 111 111 111 111 111 111 111 596
 Leu Met Lys Ile Lys Asn Gln Pro Lys Glu Arg Leu Val
 165 170 175

25 111 111 111 111 111 111 111 111 111 111 111 111 111 111 635
 Leu Ser Trp Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser
 180 185 190

30 111 111 111 111 111 111 111 111 111 111 111 111 111 111 674
 Asp Lys Asp Phe Gln Cys Leu Ile Lys Leu Leu Pro Ser
 195 200

35 111 111 111 111 111 111 111 111 111 111 111 111 111 111 713
 Cys Leu His Pro Tyr Ile Tyr Arg Val Thr Phe Ala Thr
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40 111 111 111 111 111 111 111 111 111 111 111 111 111 111 752
 Ala Asn Glu Ser Ser Ala Leu Leu Ile Arg Met Phe Asn
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45 111 111 111 111 111 111 111 111 111 111 111 111 111 111 791
 Glu Lys Gly Thr Leu Lys Asp Leu Ile Tyr Lys Ala Lys
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 Pro Lys Asp Pro Phe Leu Lys Lys Tyr Cys Asn Pro Lys
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55 111 111 111 111 111 111 111 111 111 111 111 111 111 111 869
 Lys Ile Gln Gly Leu Glu Leu Gln Gln Ile Lys Thr Tyr
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 Gly Arg Gln Ile Leu Glu Val Leu Lys Phe Leu His Asp
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 Lys Gly Phe Pro Tyr Gly His Leu His Ala Ser Asn Val
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 121 Ala Ser Thr Val Val Ser Ala Val Ser Ser Ser Thr
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5 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
 121 Ala Val Asn Gly Met Ser Arg Thr Ala Ser Ser Ser Ser
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10 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
 121 Ile Glu Asn Phe Glu Lys Gly Thr Leu Arg Lys Ala Lys
 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142

15 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
 121 Thr Cys Asp His Ser Ala Phe Lys Ile Gly
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 cctaccccc aaactacct cttccctggga aagtaattgc tgagccagta 1900
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Glu Ser His Thr Glu Tyr Ile Ile Arg Val Glu Arg Gly Ile Ser
34 38 41

10 Val Glu Asn Ser Trp Glu Ile Val Arg Arg Tyr Ser Asp Ile Asp
44 48 52

Leu Leu Asn Asn Ser Leu Glu Ile Ala Gly Leu Ser Leu Pro Leu
55 59 75

15 Pro Pro Lys Lys Leu Ile Gly Asp Met Asp Arg Glu Phe Ile Ala
80 85 90

20 Glu Arg Glu Lys Gly Leu Glu Asn Tyr Leu Asn Val Ile Thr Thr
95 100 105

Asn His Ile Leu Ser Asn Cys Glu Leu Val Lys Lys Phe Leu Asp
110 115 120

25 Pro Asn Asn Tyr Ser Ala Asn Tyr Thr Glu Ile Ala Leu Glu Glu
125 130 135

Val Ser Met Phe Phe Arg Ser Glu Pro Lys Trp Glu Val Val Glu
140 145 150

30 Pro Leu Lys Asp Ile Gly Trp Arg Ile Arg Lys Lys Tyr Phe Leu
155 160 165

35 Met Lys Ile Lys Asn Glu Pro Lys Glu Arg Leu Val Leu Ser Trp
170 175 180

Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser Asp Lys Asp Phe Glu
185 190 195

40 Cys Leu Ile Lys Leu Leu Pro Ser Cys Leu His Pro Tyr Ile Tyr
200 205 210

Arg Val Thr Phe Ala Thr Ala Asn Glu Ser Ser Ala Leu Leu Ile
215 220 225

45 Arg Met Phe Asn Glu Lys Gly Thr Leu Lys Asp Leu Ile Tyr Lys
230 235 240

50 Ala Lys Pro Lys Asp Pro Phe Leu Lys Lys Tyr Cys Asn Pro Lys
245 250 255

Lys Ile Glu Gly Leu Glu Leu Glu Glu Ile Lys Thr Tyr Gly Arg
260 265 270

55 Glu Ile Leu Glu Val Leu Lys Phe Leu His Asp Lys Gly Phe Pro
275 280 285

Tyr Gly His Leu His Ala Ser Asn Val Met Leu Asp Gly Asp Thr
290 295 300

60 Cys Arg Leu Leu Asp Leu Glu Asn Ser Leu Leu Gly Leu Pro Ser
305 310 315

	His Tyr Arg Ser Lys His Ser Ala His Arg Lys Ile Asn Ser Leu	42	425	441
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	Thr Tyr Gly Arg Ile Ile Arg Ser Val Ile Val Asp Ser Phe Ile	450	455	461
10	Ile Ala Pro Ser Met Ala Val Val Ala Val Leu Gln Ser Thr Leu	461	475	475
	Ser Cys Glu Ala Cys Lys Asn Gly Met Pro Thr Ile Ser Arg Leu	480	485	491
15	Leu Gln Met Pro Leu Phe Ser Asp Val Leu Leu Thr Thr Ser Gln	495	495	495
	Lys Pro Gln Phe Lys Ile Pro Thr Lys Leu Lys Glu Ala Leu Arg	410	415	420
20	Ile Ala Lys Glu Cys Ile Glu Lys Arg Leu Ile Glu Glu Gln Lys	425	430	435
	Gln Ile His Gln His Arg Arg Leu Thr Arg Ala Gln Ser His His	440	445	450
25	Gly Ser Glu Glu Glu Arg Lys Lys Arg Lys Ile Leu Ala Arg Lys	455	460	465
	Lys Ser Lys Arg Ser Ala Leu Glu Asn Ser Glu Glu His Ser Ala	470	475	480
30	Arg Tyr Ser Asn Ser Asn Asn Ser Gly Ser Gly Ala Ser Ser Pro	485	490	495
	Leu Thr Ser Pro Ser Ser Pro Thr Pro Pro Ser Thr Ser Gly Ile	500	505	510
35	Ser Ala Leu Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Ala Ala	515	520	525
	Pro Leu Pro Pro Ala Ser Thr Glu Val Pro Ala Gln Leu Ser Ser	530	535	540
40	Gln Ala Val Asn Gly Met Ser Arg Gly Ala Leu Leu Ser Ser Ile	545	550	555
	Gln Asn Phe Gln Lys Gly Thr Leu Arg Lys Ala Lys Thr Cys Asp	560	565	570
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Met Ala Gln His Asp Phe Val Pro Ala
 1 5 491

Trp Leu Asn Phe Ser Thr Pro Gln Ser Ala Lys Ser Pro
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Thr Ala Thr Phe Glu Lys His Gly Glu His Leu Pro Arg
 25 30 35 569

Gly Glu Gly Arg Phe Gly Val Ser Arg Arg Arg His Asn
 40 45 608

Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg Thr
 50 55 60 647

Ala Gly Asp Ser Trp His Gln Pro Ser Cys Ser Ala Met
 65 70 686

Ile Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu
 75 80 85 725

Glu Ser Gln Gly Thr His Leu Val Gly Ile Ala Leu Pro
 90 95 100 764

Arg Gly His Asp Gly Met Ser Gln Arg Ser Val Gly Gly
 105 110 803

Thr Gly Asn His Arg His Trp Asn Gly Ser Phe His Ser
 115 120 125 842

Arg Lys Gly Cys Ala Phe Gln Glu Lys Pro Pro Met Glu
 130 135 881

Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu Lys Leu
 140 145 150 920

Gln Phe Glu Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu
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8

	Leu Thr Thr Leu Val Ser Leu Arg His His Met Leu Thr Ser His	110	115
5	Lys His His Leu Val Lys Leu Arg Leu His Ser Lys His Arg His	115	120
	Met Ser His Arg Ser Val Lys Lys His Lys Asn His Arg His Thr	120	125
10	Asn Lys Ser Phe His Ser Arg Lys Lys Lys Ala Leu Glu Glu Lys	125	130
	Phe Phe Met Glu Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu	130	135
15	Lys Leu Glu Phe Glu Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu	135	140
	Ala Gly Lys Glu His Glu Pro Cys Arg Pro Ile Gly Thr Pro Ser	140	145
20	Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Glu Pro Ser Lys Met	145	150
	Leu Val Ile Lys Lys Val Ser Lys Glu Asp Pro Ala Ala Ala Phe	150	155
25	Ser Ala Ala Phe Thr Ser Pro Gly Ser His His Ala Asn Gly Asn	155	160
	Lys Leu Ser Ser Val Val Pro Ser Val Tyr Lys Asn Leu Val Pro	160	165
30	Lys Pro Val Pro Pro Pro Ser Lys Pro Asn Ala Trp Lys Ala Asn	165	170
	Arg Met Glu His Lys Ser Gly Ser Leu Ser Ser Ser Arg Glu Ser	170	175
35	Ala Phe Thr Ser Pro Ile Ser Val Thr Lys Pro Val Val Leu Ala	175	180
	Ser Gly Ala Ala Leu Ser Ser Pro Lys Glu Ser Pro Ser Ser Thr	180	185
40	Thr Pro Pro Ile Glu Ile Ser Ser Ser Arg Leu Thr Lys Leu Thr	185	190
	Arg Arg Thr Thr Asp Arg Lys Ser Glu Phe Leu Lys Thr Leu Lys	190	195
45	Arg Asp Arg Asn Gly Asp Phe Ser Glu Asn Arg Asp Cys Arg Lys	195	200
	Leu Glu Asp Leu Glu Asp Asn Ser Thr Pro Glu Pro Lys Glu Asn	200	205
50	Gly Glu Glu Gly Cys His Glu Asn Gly Leu Ala Leu Pro Val Val	205	210
	Glu Glu Gly Glu Val Leu Ser His Ser Leu Glu Ala Glu His Arg	210	215
55	Leu Leu Lys Ala Met Gly Trp Glu Glu Tyr Pro Glu Asn Asp Glu	215	220

400 401 402
 5 Asn Lys Leu Ser Lys Thr Glu Arg Glu Lys Lys Thr Ser His Met
 410 411 412
 10 Lys Thr Glu Thr Leu Arg Arg Asn Gly His Gly Lys Asn Gly His
 420 421 422
 15 Leu Glu Ser Arg Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
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 40 ggcggcaga tngtnagaag atacagtgcg tnnatntgc ttaacaaag 200
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 742, 774, 784
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 tgcctgcyttc tetgctgcac tcaacctacc aggatctcac catgcaaatg 250
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 aagcctgtac caacctcttc caagcctaai goatggaaaag ctaacaggat 350
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 Met Ser Trp Leu Ser Ser Ser
 1 5

30

cag gga gtg gln cta aca gcc tac cac ccc agc ggc aag 130
 Gln Gly Val Xaa Leu Thr Ala Tyr His Pro Ser Gly Lys
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gac cag acc gtc ggg aac agc cat gca aag gca ggg gag 169
 Asp Gln Thr Val Gly Asn Ser His Ala Lys Ala Gly Glu
 25 30

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gaa gcc acc tcg agt cgc aga tat ggc cag tac act atg 208
 Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr Met
 35 40 45

45

aac cag gaa agc acc acc atc aaa gtt atg gag aag cct 247
 Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro
 50 55

50

cca ttt gat cga tca att tcc cag gat tct ttg gat gaa 286
 Pro Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu Asp Glu
 60 65 70

55

cta tct atg gaa gac tat tgg ata gaa cta gaa aac atc 325
 Leu Ser Met Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile
 75 80 85

60

aag aaa tct agt gaa aac agc caa gaa gat caa gag gtg 364
 Lys Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln Glu Val
 90 95

gtt gtt gtc aac gac cct gat gac gaa gaa tta gaa gaa 403
 Val Val Val Lys Glu Pro Asp Glu Gly Gln Leu Glu Glu
 100 105 110

gag tgg cta aaa gag gcc ggt tta tcc aat cta tcc gga 442
 Glu Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly
 115 120

gag tct gct gga gat cca cag gaa agc att ggt tta tta 481
 Glu Ser Ala Gly Asp Pro Gln Glu Ser Ile Val Phe Leu
 125 130 135

141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156
 Ala Thr Leu Thr Arg Thr Val Ala Ala Ala Val His Lys
 141 144 147

5 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172
 Arg Val Gln Thr Val Ser Gln Thr Leu Arg Lys Lys Asn
 157 160 163

10 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188
 Lys Gln Tyr Gln Ile Arg Asp Val Arg Asp Val Arg Ala
 165 168 171

15 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204
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20 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220
 Glu Ser Gln Ser Leu Arg Thr Asn Glu Asn Lys Tyr Gln
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25 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236
 Gga aga gat gac gag gca tct aac ctt gtt ggt gaa gag 715
 Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Gln Glu
 205 208 210 215

30 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252
 aag ctg atc cca cct gag gag acg cct gcc cct gaa aca 754
 Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr
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35 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268
 gag atc aac ctg gag gta tca ttt gcc gag caa gca ctc 793
 Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu
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40 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284
 aat cag aaa gag aga tcc aag gag aaa atc cag aag agc 832
 Asn Gln Lys Glu Arg Ser Lys Glu Lys Ile Gln Lys Ser
 245 250

45 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300
 aaa ggc gat gat gcc aca tta cct agt ttc aga ttg cca 871
 Lys Gly Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro
 255 260 265

50 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316
 aaa gac aaa acg ggt acc aca agg att ggt gac ctc gca 910
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 270 275 280

55 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332
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 285 290

60 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348
 gag ctg act gcc ctc tat gat gta ttg ggt att gag ctg 988
 Glu Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu
 295 300 305

65 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364
 aaa cca cca aaa cct gtc aaa atc aaa aca aaa gat tct 1027
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 310 315

70 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380
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75 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396
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 Asp Gln Arg Lys Val Pro Gly Met Arg Ile Pro Leu Ile
 335 340 345

1

 α, β, γ

225

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400

4:5

425

440

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(ii)

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Lys Met Ala Tyr Asp Arg His Lys Tyr Glu Lys His Asp
 575 580 585 590 595 600 605 610 615 620

Lys Ser Thr Asn Asp Ala Asp Val Leu Gln Gly Val Ile
 625 630 635 640 645 650 655 660 665 670

Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala
 675 680 685 690 695 700 705 710 715 720 725

Ala Leu Thr Asn Asp Ala Asp Val Leu Gln Gly Val Ile
 730 735 740 745 750 755 760 765 770 775 780

Gln Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala
 785 790 795 800 805 810 815 820 825 830 835

Ala Leu Thr Asn Asp Ala Asp Val Leu Gln Gly Val Ile
 840 845 850 855 860 865 870 875 880 885 890

Ala Arg Phe Leu Ser Gln Glu Ser Gly Val Ala Gln Thr
 895 900 905 910 915 920 925 930 935 940 945

Cys Arg Phe Leu Ser Gln Glu Ser Gly Val Ala Gln Thr
 950 955 960 965 970 975 980 985 990 995 1000

Lys Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val
 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055

Ile Lys Ser Lys Pro Leu
 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110

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<210> 14
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His Pro Ser Gly Lys Asp Gln Thr Val Gly Asn Ser His Ala Lys
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Ala Gly Glu Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr
 35 40 45

Met Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro

	His Asp Arg Ser	100	Val Ser Thr Asp Ser Ile Asp Gln Leu Ser Met	100
5	Gln Asp Tyr Trp	110	Gln Leu Gln Asp Ile Lys Lys Ser Ser Gln	110
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	Gln Gly Gln Leu Gln Gln Thr Asp Leu Lys Gln Ala Gly Leu Ser	130	130	130
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 1 5
 gcc ggc aag gtg ctg ctg gac gac acg gtg ccg ctg aca 128
 Ala Gly Lys Val Leu Leu Asp Asp Thr Val Pro Leu Thr
 10 15 20
 gca gcc atc gag gcg agc cag agc ctg cag tcc cac acg 167
 Ala Ala Ile Glu Ala Ser Gln Ser Leu Gln Ser His Thr
 25 30
 gaa tat att att cga gtg caa aga gga att tct gtg gaa 206
 Glu Tyr Ile Ile Arg Val Gln Arg Gly Ile Ser Val Glu
 35 40 45
 aac agc tgg cag att gtt aga aga tac agt gac ttt gat 245
 Asn Ser Trp Gln Ile Val Arg Arg Tyr Ser Asp Phe Asp
 50 55 60
 ttg ctt aac aac agc tta cag att gca ggc cta agt cta 284
 Leu Leu Asn Asn Ser Leu Gln Ile Ala Gly Leu Ser Leu
 65 70
 cct ctt cct ccc aaa aaa ttg att ggt aac atg gat cgt 323
 Pro Leu Pro Pro Lys Lys Leu Ile Gly Asn Met Asp Arg
 75 80 85
 gaa ttc ata gct gaa agg cag aaa ggt ctt cag aac tat 362
 Glu Phe Ile Ala Glu Arg Gln Lys Gly Leu Gln Asn Tyr
 90 95

ctc aac gtg atc aca aca aat cat atc ttg tct aat tgt 401
 Leu Asn Val Ile Thr Thr Asn His Ile Leu Ser Asn Cys
 100 105 110

gag ctg gtt aag aag ttt tta gat cca aac aac tat tcc 440
 Glu Leu Val Lys Lys Phe Leu Asp Pro Asn Asn Tyr Ser
 115 120 125

gca aac tat act gag att gcc ttg caa cag gtt tcc atg 479
 Ala Asn Tyr Thr Glu Ile Ala Leu Gln Gln Val Ser Met
 130 135

ttc ttc cga tca gaa cca aag tgg gag gtg gtg gaa cct 518
 Phe Phe Arg Ser Glu Pro Lys Trp Glu Val Val Glu Pro
 140 145 150

ttg aaa gac ata ggt tgg aga ata agg aag aaa tat ttc 557
 Leu Lys Asp Ile Gly Trp Arg Ile Arg Lys Lys Tyr Phe
 155 160

ttg atg aag att aaa aat cag cca aag gaa cgg cta gtg 596
 Leu Met Lys Ile Lys Asn Gln Pro Lys Glu Arg Leu Val
 165 170 175

tta agc tgg gct gac ctt ggc cca gac aag tat ttg tca 635
 Leu Ser Trp Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser
 180 185 190

gat aaa gat ttt cag tgt cta atc aaa ctt ctg cct tct 674
 Asp Lys Asp Phe Gln Cys Leu Ile Lys Leu Leu Pro Ser
 195 200

tgt ttg cac cct tac atc tat cgg gtt acc ttt gcc aca 713
 Cys Leu His Pro Tyr Ile Tyr Arg Val Thr Phe Ala Thr
 205 210 215

gct aat gaa tcc tca gcg ttg cta att agg atg ttt aac 752
 Ala Asn Glu Ser Ser Ala Leu Leu Ile Arg Met Phe Asn
 220 225

gaa aag gga aca ttg aag gat ctg atc tac aag gca aaa 791
 Glu Lys Gly Thr Leu Lys Asp Leu Ile Tyr Lys Ala Lys
 230 235 240

cca aaa gac cca ttt cta aag aag tac tgc aac cct aag 830
 Pro Lys Asp Pro Phe Leu Lys Lys Tyr Cys Asn Pro Lys
 245 250 255

aag att cag gcc ctg gaa ctg cag caa ata aaa aca tat 869
 Lys Ile Gln Gly Leu Glu Leu Gln Gln Ile Lys Thr Tyr
 260 265

gga cgg caa ata tta gag gta ctg aag ttt ctt cat gac 908
 Gly Arg Gln Ile Leu Glu Val Leu Lys Phe Leu His Asp
 270 275 280

aag gga ttc cct tat ggg cat ctt cac gcc tcc aat gtg 947
 Lys Gly Phe Pro Tyr Gly His Leu His Ala Ser Asn Val
 285 290

atg ctc gat ggg gac act tgt cgg ctg ctg gac ctt gag 985
Met Leu Asp Gly Asp Thr Cys Arg Leu Leu Asp Leu Glu
295 300 305

aat tcc tta ttg ggc ctg cct tcc ttc tac cga tct tat 1025
Asn Ser Leu Leu Gly Leu Pro Ser Phe Tyr Arg Ser Tyr
310 315 320

ttt tca caa ttc agg aaa atc aat aca ttg gaa agt gtg 1064
Phe Ser Gln Phe Arg Lys Ile Asn Thr Leu Glu Ser Val
325 330

gat gtc cac tgc ttt ggc cac tta ctg tat gaa atg act 1103
Asp Val His Cys Phe Gly His Leu Leu Tyr Glu Met Thr
335 340 345

tat gga cga cgg cca gac tgc gtg cct gtg gac tcc ttc 1142
Tyr Gly Arg Pro Pro Asp Ser Val Pro Val Asp Ser Phe
350 355

cct cct gcc cgg tcc atg gct gtg gtg gcc gtg ttg gag 1181
Pro Pro Ala Pro Ser Met Ala Val Val Ala Val Leu Glu
360 365 370

tct acg ctg tct tgt gaa gcc tgt aaa aat ggc atg cct 1220
Ser Thr Leu Ser Cys Glu Ala Cys Lys Asn Gly Met Pro
375 380 385

acc atc tcc cgg ctc tta cag atg cca tta ttc agc gat 1259
Thr Ile Ser Arg Leu Leu Gln Met Pro Leu Phe Ser Asp
390 395

gtt tta cta acc act tct gaa aaa cca cag ttt aag atc 1298
Val Leu Leu Thr Thr Ser Glu Lys Pro Gln Phe Lys Ile
400 405 410

cct aca aag tta aaa gag gca ttg aga att gcc aaa gaa 1337
Pro Thr Lys Leu Lys Glu Ala Leu Arg Ile Ala Lys Glu
415 420

tgt ata gag aag aga cta att gag gaa cag aaa cag att 1376
Cys Ile Glu Lys Arg Leu Ile Glu Glu Gln Lys Gln Ile
425 430 435

cac cag cat cga aga ctg aca aga gct cag tcc cac cat 1415
His Gln His Arg Arg Leu Thr Arg Ala Gln Ser His His
440 445 450

gga tct gag gag gaa aga aaa aaa aga aag att tta gct 1454
Gly Ser Glu Glu Glu Arg Lys Lys Arg Lys Ile Leu Ala
455 460

cga aag aag tca aaa cga tct gct ctt gaa aat agt gaa 1493
Arg Lys Lys Ser Lys Arg Ser Ala Leu Glu Asn Ser Glu
465 470 475

gag cat tca gcg agg tac agc aac tcc aat aat tca gga 1532
Glu His Ser Ala Arg Tyr Ser Asn Ser Asn Asn Ser Gly
480 485

tct ggg gcc agc tca cct ctc acg tcc cgg tca tgc cca 1571

Ser Gly Ala Ser Ser Pro Leu Thr Ser Pro Ser Ser Pro
490 495 500

act cca ccc tct aca tca ggg ata tct gca tta cct cca 1610
Thr Pro Pro Ser Thr Ser Gly Ile Ser Ala Leu Pro Pro
505 510 515

cct cct cca cct cca cca cca cca gca gct ccc ttg cct 1649
Pro Pro Pro Pro Pro Pro Pro Pro Ala Ala Pro Leu Pro
520 525

cct ggg agc acc gag gta cct gcc cag ctg tgg tct cag 1688
Pro Ala Ser Thr Glu Val Pro Ala Gln Leu Ser Ser Gln
530 535 540

gct gtg aat ggc atg agc cga ggg gcc ttg ctg agc tcc 1727
Ala Val Asn Gly Met Ser Arg Gly Ala Leu Leu Ser Ser
545 550

atc cag aat ttc caa aaa gga act ttg agg aaa gcc aaa 1766
Ile Gln Asn Phe Gln Lys Gly Thr Leu Arg Lys Ala Lys
555 560 565

acc tgt gat cac agt gct ccg aag atc ggc tg aa 1800
Thr Cys Asp His Ser Ala Pro Lys Ile Gly
570 575 577

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cctaccccc aaactacct ctctctggga aagtaattgc tgagccagta 1900
cagccacaaa cagtactatt ttgcagatgc tcatgtaagc agcttttcga 1950
gagaaataat tctttaagca gaataaagtt aggcctggcat tgctccctta 2000
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 <212> PRT
 <213> Homo sapiens

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 Gln Ser His Thr Glu Tyr Ile Ile Arg Val Gln Arg Gly Ile Ser
 35 40 45
 Val Glu Asn Ser Trp Gln Ile Val Arg Arg Tyr Ser Asp Phe Asp
 50 55 60
 Leu Leu Asn Asn Ser Leu Gln Ile Ala Gly Leu Ser Leu Pro Leu
 65 70 75
 Pro Pro Lys Lys Leu Ile Gly Asn Met Asp Arg Glu Phe Ile Ala
 80 85 90
 Glu Arg Gln Lys Gly Leu Gln Asn Tyr Leu Asn Val Ile Thr Thr
 95 100 105
 Asn His Ile Leu Ser Asn Cys Glu Leu Val Lys Lys Phe Leu Asp
 110 115 120
 Pro Asn Asn Tyr Ser Ala Asn Tyr Thr Glu Ile Ala Leu Gln Gln
 125 130 135
 Val Ser Met Phe Phe Arg Ser Glu Pro Lys Trp Glu Val Val Glu
 140 145 150
 Pro Leu Lys Asp Ile Gly Trp Arg Ile Arg Lys Lys Tyr Phe Leu
 155 160 165
 Met Lys Ile Lys Asn Gln Pro Lys Glu Arg Leu Val Leu Ser Trp
 170 175 180
 Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser Asp Lys Asp Phe Gln
 185 190 195
 Cys Leu Ile Lys Leu Leu Pro Ser Cys Leu His Pro Tyr Ile Tyr
 200 205 210
 Arg Val Thr Phe Ala Thr Ala Asn Glu Ser Ser Ala Leu Leu Ile
 215 220 225

Arg Met Phe Asn Glu Lys Gly Thr Leu Lys Asp Leu Ile Tyr Lys	230	235	240
Ala Lys Pro Lys Asp Pro Phe Leu Lys Lys Tyr Cys Asn Pro Lys	245	250	255
Lys Ile Gln Gly Leu Glu Leu Gln Gln Ile Lys Thr Tyr Gly Arg	260	265	270
Gln Ile Leu Glu Val Leu Lys Phe Leu His Asp Lys Gly Phe Pro	275	280	285
Tyr Gly His Leu His Ala Ser Asn Val Met Leu Asp Gly Asp Thr	290	295	300
Cys Arg Leu Leu Asp Leu Glu Asn Ser Leu Leu Gly Leu Pro Ser	305	310	315
Phe Tyr Arg Ser Tyr Phe Ser Gln Phe Arg Lys Ile Asn Thr Leu	320	325	330
Glu Ser Val Asp Val His Cys Phe Gly His Leu Leu Tyr Glu Met	335	340	345
Thr Tyr Gly Arg Pro Pro Asp Ser Val Pro Val Asp Ser Phe Pro	350	355	360
Pro Ala Pro Ser Met Ala Val Val Ala Val Leu Glu Ser Thr Leu	365	370	375
Ser Cys Glu Ala Cys Lys Asn Gly Met Pro Thr Ile Ser Arg Leu	380	385	390
Leu Gln Met Pro Leu Phe Ser Asp Val Leu Leu Thr Thr Ser Glu	395	400	405
Lys Pro Gln Phe Lys Ile Pro Thr Lys Leu Lys Glu Ala Leu Arg	410	415	420
Ile Ala Lys Glu Cys Ile Glu Lys Arg Leu Ile Glu Glu Gln Lys	425	430	435
Gln Ile His Gln His Arg Arg Leu Thr Arg Ala Gln Ser His His	440	445	450
Gly Ser Glu Glu Glu Arg Lys Lys Arg Lys Ile Leu Ala Arg Lys	455	460	465
Lys Ser Lys Arg Ser Ala Leu Glu Asn Ser Glu Glu His Ser Ala	470	475	480
Arg Tyr Ser Asn Ser Asn Asn Ser Gly Ser Gly Ala Ser Ser Pro	485	490	495
Leu Thr Ser Pro Ser Ser Pro Thr Pro Pro Ser Thr Ser Gly Ile	500	505	510
Ser Ala Leu Pro Pro Pro Pro Pro Pro Pro Pro Pro Ala Ala	515	520	525
Pro Leu Pro Pro Ala Ser Thr Glu Val Pro Ala Gln Leu Ser Ser			

530

535

540

Gln Ala Val Asn Gly Met Ser Arg Gly Ala Leu Leu Ser Ser Ile
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Gln Asn Phe Gln Lys Gly Thr Leu Arg Lys Ala Lys Thr Cys Asp
560 565 570

His Ser Ala Pro Lys Ile Gly
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<211> 2119

<212> DNA

<213> Homo sapiens

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gtgaacatag atacagctct ttccccctcc cccctttttt aaatgtaaca 150
aatacttttt atgttcccc tcccccttc cctttttccc ctttccccct 200
ttggaaaagt gtcaggaacc aaatagttaa agatgagcag ttgaggggac 250
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cgtgctgccg gccagggttac ttaagcacc ttttaacaag gaaaccttgt 350
gggagatcca gctggccgac tcgagttcag aaacaggacc acagagggtta 400
cactctggga tcctggccat gaggttggat gcctcacctt actgaaagga 450
gacactggac ctaa atg gcg cag cat gat ttt gtt cct gct 491
Met Ala Gln His Asp Phe Val Pro Ala

1

5

tgg cta aat ttc tca aca cca cag tca gct aag tca cct 530
Trp Leu Asn Phe Ser Thr Pro Gln Ser Ala Lys Ser Pro
10 15 20

act gcc acc ttc gaa aaa cac gga gag cac cta ccc aga 565
Thr Ala Thr Phe Glu Lys His Gly Glu His Leu Pro Arg
25 30 35

gga gaa ggt aga ttt gga gta agc cgc cgt cga cat aat 600
Gly Glu Gly Arg Phe Gly Val Ser Arg Arg Arg His Asn
40 45

tcc tct gat ggt ttt ttt aac aat ggt ccc cta cga act 647
Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg Thr
50 55 60

gca gga gat tct tgg cac cag ccc tcc tgt tcc gcc atg 685
Ala Gly Asp Ser Trp His Gln Pro Ser Cys Ser Ala Met
65 70

att ctg tgg act ctg gtg tct cta agg gag cat atg ctg 725
Ile Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu

75

80

85

gaa tca cag gga acc cat ctg gtt ggc ata gct ctt ccc 764
 Glu Ser Gln Gly Thr His Leu Val Gly Ile Ala Leu Pro
 90 95 100

cga ggt cat gat ggc atg agc caa cgt agt gta ggt ggc 803
 Arg Gly His Asp Gly Met Ser Gln Arg Ser Val Gly Gly
 105 110

aca ggg aac cat cgc cat tgg aat ggc agt ttc cac tcc 842
 Thr Gly Asn His Arg His Trp Asn Gly Ser Phe His Ser
 115 120 125

cgg aaa ggg tgt gct ttt cag gaa aag cca cct atg gag 881
 Arg Lys Gly Cys Ala Phe Gln Glu Lys Pro Pro Met Glu
 130 135

att agg gaa gaa aag aaa gaa gac aag gtg gaa aag ttg 920
 Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu Lys Leu
 140 145 150

cag ttt gaa gag gag gac ttt cct tcc ttg aat cca gaa 959
 Gln Phe Glu Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu
 155 160 165

gct ggc aaa cag cat cag cca tgc aga cct att ggg aca 998
 Ala Gly Lys Gln His Gln Pro Cys Arg Pro Ile Gly Thr
 170 175

cct tct gga gta tgg gaa aac ccg cct agt gcc aag caa 1037
 Pro Ser Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Gln
 180 185 190

ccc tcc aag atg cta gtt atc aaa aaa gtt tcc aaa gag 1076
 Pro Ser Lys Met Leu Val Ile Lys Lys Val Ser Lys Glu
 195 200

gat cct gct gct gcc ttc tct gct gca ttc acc tca cca 1115
 Asp Pro Ala Ala Ala Phe Ser Ala Ala Phe Thr Ser Pro
 205 210 215

gga tct cac cat gca aat ggg aac aaa ttg tca tcc gtg 1154
 Gly Ser His His Ala Asn Gly Asn Lys Leu Ser Ser Val
 220 225 230

gtt cca agt gtc tat aag aac ctg gtt cct aag cct gta 1193
 Val Pro Ser Val Tyr Lys Asn Leu Val Pro Lys Pro Val
 235 240

cca cct cct tcc aag cct aat gca tgg aaa gct aac agg 1232
 Pro Pro Pro Ser Lys Pro Asn Ala Trp Lys Ala Asn Arg
 245 250 255

atg gag cac aag tca gga tcc ctt tcc tct agc cgg gag 1271
 Met Glu His Lys Ser Gly Ser Leu Ser Ser Ser Arg Glu
 260 265

tct gct ttt acc agt cca atc tcc gtt acc aaa cca gtg 1310
 Ser Ala Phe Thr Ser Pro Ile Ser Val Thr Lys Pro Val
 270 275 280

gta ctg gct agt ggt gca gct ctg agt tct ccc aaa gag 1349
 Val Leu Ala Ser Gly Ala Ala Leu Ser Ser Pro Lys Glu
 285 290 295

agt ccc tcc agc acc acc cct cca att gag atc agc tcc 1388
 Ser Pro Ser Ser Thr Thr Pro Pro Ile Glu Ile Ser Ser
 300 305

tct cgt ctg acc aag ttg acc cgc cga acc acc gac agg 1427
 Ser Arg Leu Thr Lys Leu Thr Arg Arg Thr Thr Asp Arg
 310 315 320

aag agt gag ttc ctg aaa act ctg aag gat gac cgg aat 1466
 Lys Ser Glu Phe Leu Lys Thr Leu Lys Asp Asp Arg Asn
 325 330

gga gac ttc tca gag aat aga gac tgt qac aag ctg gaa 1505
 Gly Asp Phe Ser Glu Asn Arg Asp Cys Asp Lys Leu Glu
 335 340 345

gat ttg gag gac aac agc aca cct gaa cca aag gaa aat 1544
 Asp Leu Glu Asp Asn Ser Thr Pro Glu Pro Lys Glu Asn
 350 355 360

ggg gag gaa ggc tgt cat caa aat ggt ctt gcc ctc cct 1583
 Gly Glu Glu Gly Cys His Gln Asn Gly Leu Ala Leu Pro
 365 370

gta gtg gaa gaa ggg gag gtt ctc tca cac tct cta gaa 1622
 Val Val Glu Glu Gly Glu Val Leu Ser His Ser Leu Glu
 375 380 385

gca gag cac agg tta ttg aaa gct atg ggt tgg cag gaa 1661
 Ala Glu His Arg Leu Leu Lys Ala Met Gly Trp Gln Glu
 390 395

tat cct gaa aat gat gag aat tgc ctt ccc ctc aca gag 1700
 Tyr Pro Glu Asn Asp Glu Asn Cys Leu Pro Leu Thr Glu
 400 405 410

gat gag ctc aaa gag ttc cac atg aag aca gag cag ctg 1739
 Asp Glu Leu Lys Glu Phe His Met Lys Thr Glu Gln Leu
 415 420 425

aga aga aat ggc ttt gga aag aat ggc ttc ttg cag agc 1778
 Arg Arg Asn Gly Phe Gly Lys Asn Gly Phe Leu Gln Ser
 430 435

cgc agt tcc agt ctg ttc tcc cct tgg aga agc act tgc 1817
 Arg Ser Ser Ser Leu Phe Ser Pro Trp Arg Ser Thr Cys
 440 445 450

aaa gca gag ttt gag gac tca gac acc gaa acc agt agc 1856
 Lys Ala Glu Phe Glu Asp Ser Asp Thr Glu Thr Ser Ser
 455 460

agt gaa aca tca gat gac gat gcc tgg aag t agg 1890
 Ser Glu Thr Ser Asp Asp Ala Trp Lys
 465 470 474

catataaatg ctccacagtta aatctgaccc actaaaactct gtgtgttttag 1940
 ggagtataca aaagaaatcg ttcttttctt tttcttatgt tgttgaatac 1990
 ttcattcaca agggaaataa tcatatccca aagagagaaa aaaaaaaaaa 2040
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 ataagcttgg cgcgcattgg ccaacttgt 2119

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 Glu His Leu Pro Arg Gly Glu Gly Arg Phe Gly Val Ser Arg Arg
 35 40 45
 Arg His Asn Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg
 50 55 60
 Thr Ala Gly Asp Ser Trp His Gln Pro Ser Cys Ser Ala Met Ile
 65 70 75
 Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu Glu Ser Gln
 80 85 90
 Gly Thr His Leu Val Gly Ile Ala Leu Pro Arg Gly His Asp Gly
 95 100 105
 Met Ser Gln Arg Ser Val Gly Gly Thr Gly Asn His Arg His Trp
 110 115 120
 Asn Gly Ser Phe His Ser Arg Lys Gly Cys Ala Phe Gln Glu Lys
 125 130 135
 Pro Pro Met Glu Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu
 140 145 150
 Lys Leu Gln Phe Glu Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu
 155 160 165
 Ala Gly Lys Gln His Gln Pro Cys Arg Pro Ile Gly Thr Pro Ser
 170 175 180
 Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Gln Pro Ser Lys Met
 185 190 195
 Leu Val Ile Lys Lys Val Ser Lys Glu Asp Pro Ala Ala Ala Phe
 200 205 210
 Ser Ala Ala Phe Thr Ser Pro Gly Ser His His Ala Asn Gly Asn
 215 220 225

Lys	Leu	Ser	Ser	Val	Val	Pro	Ser	Val	Tyr	Lys	Asn	Leu	Val	Pro	230	235	240
Lys	Pro	Val	Pro	Pro	Pro	Ser	Lys	Pro	Asn	Ala	Trp	Lys	Ala	Asn	245	250	255
Arg	Met	Glu	His	Lys	Ser	Gly	Ser	Leu	Ser	Ser	Ser	Arg	Glu	Ser	260	265	270
Ala	Phe	Thr	Ser	Pro	Ile	Ser	Val	Thr	Lys	Pro	Val	Val	Leu	Ala	275	280	285
Ser	Gly	Ala	Ala	Leu	Ser	Ser	Pro	Lys	Glu	Ser	Pro	Ser	Ser	Thr	290	295	300
Thr	Pro	Pro	Ile	Glu	Ile	Ser	Ser	Ser	Arg	Leu	Thr	Lys	Leu	Thr	305	310	315
Arg	Arg	Thr	Thr	Asp	Arg	Lys	Ser	Glu	Phe	Leu	Lys	Thr	Leu	Lys	320	325	330
Asp	Asp	Arg	Asn	Gly	Asp	Phe	Ser	Glu	Asn	Arg	Asp	Cys	Asp	Lys	335	340	345
Leu	Glu	Asp	Leu	Glu	Asp	Asn	Ser	Thr	Pro	Glu	Pro	Lys	Glu	Asn	350	355	360
Gly	Glu	Glu	Gly	Cys	His	Gln	Asn	Gly	Leu	Ala	Leu	Pro	Val	Val	365	370	375
Glu	Glu	Gly	Glu	Val	Leu	Ser	His	Ser	Leu	Glu	Ala	Glu	His	Arg	380	385	390
Leu	Leu	Lys	Ala	Met	Gly	Trp	Gln	Glu	Tyr	Pro	Glu	Asn	Asp	Glu	395	400	405
Asn	Cys	Leu	Pro	Leu	Thr	Glu	Asp	Glu	Leu	Lys	Glu	Phe	His	Met	410	415	420
Lys	Thr	Glu	Gln	Leu	Arg	Arg	Asn	Gly	Phe	Gly	Lys	Asn	Gly	Phe	425	430	435
Leu	Gln	Ser	Arg	Ser	Ser	Ser	Leu	Phe	Ser	Pro	Trp	Arg	Ser	Thr	440	445	450
Cys	Lys	Ala	Glu	Phe	Glu	Asp	Ser	Asp	Thr	Glu	Thr	Ser	Ser	Ser	455	460	465
Glu	Thr	Ser	Asp	Asp	Asp	Ala	Trp	Lys							470		

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<111> 294

<112> DNA

<113> Homo sapiens

<110>

<111> unsure

<112> 162, 165, 183-184, 187, 204, 207, 211, 216, 219, 222-223, 225, 237, 240, 244, 250, 253, 262, 267, 269, 275, 279, 282, 289-290

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 cacacacgggtg ccqctgacag cagccatcga ggcgagccag agcctgcagt 100
 cacacacgga atatattatt cgagtgcataa gaqqaatttc tctggaaaac 150
 auctggcaga tngtnagaag atacagtgaac tnnnatntgc ttaacaacag 200
 cttncaanatt ncaggncina gnnntcctct tctctcnaaa aaantgattn 250
 ggnaacatgg ancgtnant tcatngctng anaggcagnn aggt 294

<210> 6
 <211> 24
 <212> DNA
 <213> Homo sapiens

<400> 6
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<210> 7
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 7
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a 51

<210> 8
 <211> 31
 <212> DNA
 <213> Homo sapiens

<400> 8
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<210> 9
 <211> 793
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 379, 433, 459, 492, 517, 541, 549, 561, 575, 579, 582, 710, 742,
 774, 784
 <223> unknown base

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 gacctattgg gacaccttct ggagtatggg aaaaaccgccc tagtgccaag 150
 caaccctcca agatgctagt tatcaaaaaa gtttccaaag aggatcctgc 200
 tgctgcyytc tctgctgcat tcacctcacc aggatctcac catgcaaag 250

ggaacaaatt gtcacccgtg gttccaagt tctataagaa cctgggttct 300
 aagcctgtac caccctcttc caagcctaata gcatggaaag ctaacaggat 350
 ggaagacaag tcaggatccc ttctctctna gccgggagtc tgtttttacc 400
 attccaatct ctgttaccaa accagtggtg ctnggctaqt ggtgcagctc 450
 tcagttctnc ccaaagagag tccctccagc accacccctc cnaattgaga 500
 ttagctcttc tctctngac caagtttgac ccgcggaacc naccgacang 550
 gaagragtga ngttcctgaa aactnctgna anggatgacc gggaatggga 600
 agacttcttc agaagaatag agactgtgac aagctggaag atttggagga 650
 caacagcaca ctgaaccaa ggaaaatggg ggaggaaggc tgttcatcaa 700
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<210> 13
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 agtatgtccc ttctctcacc atg agc tgg ctc tcc agt tcc 91

Met Ser Trp Leu Ser Ser Ser

1

5

cag gga gtg gtn cta aca gcc tac cac ccc agc qgc aag 130
Gln Gly Val Xaa Leu Thr Ala Tyr His Pro Ser Gly Lys
10 15 20

gac cag acc gtc qgg aac agc cat gca aag gca ggg gag 169
Asp Gln Thr Val Gly Asn Ser His Ala Lys Ala Gly Glu
25 30

gaa gcc acc tcg agt cgc aga tat gcc cag tac act atg 208
Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr Met
35 40 45

aac cag gaa agc acc acc atc aaa gtt atg gag aag cct 247
Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro
50 55

cca ttt gat cga tca att tcc cag gat tct ttg gat gaa 286
Pro Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu Asp Glu
60 65 70

cta tct atg gaa gac tat tgg ata gaa cta gaa aac atc 325
Leu Ser Met Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile
75 80 85

aag aaa tct agt gaa aac agc caa gaa gat caa gag gtg 364
Lys Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln Glu Val
90 95

gtt gtt gtc aaa gag cct gat gag gga gaa ttg gaa gaa 403
Val Val Val Lys Glu Pro Asp Glu Gly Glu Leu Glu Glu
100 105 110

gag tgg ctt aaa gag gcc ggt tta tcc aat ctc ttc gga 442
Glu Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly
115 120

gag tct gct gga gat cca cag gaa agc att gtg ttt tta 481
Glu Ser Ala Gly Asp Pro Gln Glu Ser Ile Val Phe Leu
125 130 135

tca aca ttg acg cgg acc cag gca gca gca gtt cag aag 520
Ser Thr Leu Thr Arg Thr Gln Ala Ala Ala Val Gln Lys
140 145 150

cga gta gag acg gtc tcc cag acc ttg agg aaa aaa aac 559
Arg Val Glu Thr Val Ser Gln Thr Leu Arg Lys Lys Asn
155 160

aaa cag tac cag att cct gac gtc aga gac ata ttt gct 598
Lys Gln Tyr Gln Ile Pro Asp Val Arg Asp Ile Phe Ala
165 170 175

caa cag aga gaa tca aaa gaa aca gct cca ggt gcc act 637
Gln Gln Arg Glu Ser Lys Glu Thr Ala Pro Gly Gly Thr
180 185

gaa tcg cag tca ctt aga aca aat gaa aac aaa tac caa 676
Glu Ser Gln Ser Leu Arg Thr Asn Glu Asn Lys Tyr Gln

190

195

200

gga aga gat gac gag gca tct aac ctt gtt ggt gaa gag 715
 Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Glu Glu
 205 210 215

aag ctg atc cca cct gag qag acg cct gcc cct gaa aca 754
 Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr
 220 225

gac atc aac ctg gag gta tca ttt gcc gag caa qca ctc 793
 Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu
 230 235 240

aat cag aaa gag aga tcc aag gag aaa atc cag aag agc 832
 Asn Gln Lys Lys Arg Ser Lys Glu Lys Ile Gln Lys Ser
 245 250

aaa ggc gat gat gcc aca tta cct agt ttc aga ttg cca 871
 Lys Gly Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro
 255 260 265

aaa gac aaa acg ggt acc aca agg att ggt gac ctc gca 910
 Lys Asp Lys Thr Gly Thr Thr Arg Ile Gly Asp Leu Ala
 270 275 280

ccc cag gac atg aag aaa gtt tgc cat tta gcc cta att 949
 Pro Gln Asp Met Lys Lys Val Cys His Leu Ala Leu Ile
 285 290

gag ctg act gcc ctc tat gat gta ttg ggt att gag ctg 988
 Glu Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu
 295 300 305

aaa caa caa aaa gct gtg aaa atc aaa aca aaa gat tct 1027
 Lys Gln Gln Lys Ala Val Lys Ile Lys Thr Lys Asp Ser
 310 315

ggt ctt ttt tgc gtt cca ttg aca gcg cta tta gaa caa 1056
 Gly Leu Phe Cys Val Pro Leu Thr Ala Leu Leu Glu Gln
 320 325 330

gat cag agg aaa gta cca gga atg cga ata ccc ttg atc 1105
 Asp Gln Arg Lys Val Pro Gly Met Arg Ile Pro Leu Ile
 335 340 345

ttt caa aaa ctg att tct cga att gaa gag aga ggt ttg 1144
 Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu
 350 355

gaa aca gaa ggc ctc tta cgg atc cct gga gct gcc att 1183
 Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile
 360 365 370

aga atc aag aat ctt tgc caa gaa cta gaa gca aag ttt 1222
 Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe
 375 380

tat gaa ggg act ttt aat tgg gaa agt gtc aaa cag cat 1261
 Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His
 385 390 395

gat gcc gcc agc ctg ctg aag ctc ttc att cgg gag ttg 1300
 Asp Ala Ala Ser Leu Leu Lys Leu Phe Ile Arg Glu Leu
 400 405 410

ccc cag cca ctg ctc agt gtg gag tat ctc aaa gcc ttt 1339
 Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu Lys Ala Phe
 415 420

cag gct gtc cag aat ctt cca acc aag aag cag caa cta 1378
 Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln Leu
 425 430 435

cag gct ttg aac ctt ctt gtc atc ctc cta cct gat gca 1417
 Gln Ala Leu Asn Leu Leu Val Ile Leu Leu Pro Asp Ala
 440 445

aac agg gac aca ctg aag gcc ctt ctt gaa ttt ctc caa 1456
 Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln
 450 455 460

aga gta ata gat aat aaa gaa aaa aat aaa atg aca gtc 1495
 Arg Val Ile Asp Asn Lys Glu Lys Asn Lys Met Thr Val
 465 470 475

atg aat gta gca atg gtc atg gcc ccg aat ctc ttt atg 1534
 Met Asn Val Ala Met Val Met Ala Pro Asn Leu Phe Met
 480 485

tgt cat gca ttg gga ttg aag tcc agt gaa cag cga gaa 1573
 Cys His Ala Leu Gly Leu Lys Ser Ser Glu Gln Arg Glu
 490 495 500

ttt gta atg gca gct ggg aca gca aat acc atg cac tta 1612
 Phe Val Met Ala Ala Gly Thr Ala Asn Thr Met His Leu
 505 510

ttg att aag tac caa aaa ctt ctg tgg aca att ccc aag 1651
 Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile Pro Lys
 515 520 525

ttt att gta aac caa gtg agg aag caa aac acg gaa aat 1690
 Phe Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn
 530 535 540

cat aaa aag gat aaa aga gcc atg aag aaa ttg ctg aag 1729
 His Lys Lys Asp Lys Arg Ala Met Lys Lys Leu Leu Lys
 545 550

aaa atg gct tat gac cga gaa aaa tat gaa aag caa gat 1768
 Lys Met Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp
 555 560 565

aag agt aca aat gat gct gac gtt cct cag gga gtg att 1807
 Lys Ser Thr Asn Asp Ala Asp Val Pro Gln Gly Val Ile
 570 575

cga gtg caa gct ccc cat ctt tgg aaa gtt tcc atg gca 1846
 Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala
 580 585 590

ata cag cta act gaa gaa cta aaa gcc agt gat gta ctt 1885
 ile gln leu thr glu glu leu lys ala ser asp val leu
 595 600 605

gcc agg ttt ctc agc caa gaa agt ggg gtt gcc cag act 1924
 ala arg phe leu ser gln glu ser gly val ala gln thr
 610 615

ctc aag aaa gga gaa gtt ttt ttg tat gaa att gga gga 1963
 leu lys lys gly glu val phe leu tyr glu ile gly gly
 620 625 630

aat att ggg gaa cgc tgc ctt gat gat gac act tac atg 2002
 asn ile gly glu arg cys leu asp asp asp thr tyr met
 635 640

aag gat tta tat cag ctt aac cca aat gct gag tgg gtt 2041
 lys asp leu tyr gln leu asn pro asn ala glu trp val
 645 650 655

ata aag tca aag cca ttg t agaagactta acaagctgca 2080
 ile lys ser lys pro leu
 660 663

gataaccatg tggactttctg tcataattct tgctgagtca agagtgtaaa 2130
 taaaagaaat ggcaggactc atattattca gttgtacca agtattttta 2180
 aaatgactct cttaagcctt aaaaagtcac agatttgtgc tgctgccaga 2230
 attatattaa attattatta atggtattat tagaaaaaaa aatttctgga 2280
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<111> 663

<112> PRT

<113> Homo sapiens

<400> 14

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Ala Gly Glu Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr
 35 40 45

Met Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro
 50 55 60

Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met
 65 70 75

Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu
 80 85 90

Asn Ser Gln Glu Asp Gln Glu Val Val Val Val Lys Glu Pro Asp

95	100	105
Glu Gly Glu Leu Glu Glu Glu Trp Leu	Lys Glu Ala Gly Leu Ser	110
110	115	
Asn Leu Phe Gly Glu Ser Ala Gly Asp	Pro Gln Glu Ser Ile Val	125
125	130	
Phe Leu Ser Thr Leu Thr Arg Thr Gln	Ala Ala Ala Val Gln Lys	150
140	145	
Arg Val Glu Thr Val Ser Gln Thr Leu	Arg Lys Lys Asn Lys Gln	165
155	160	
Tyr Gln Ile Pro Asp Val Arg Asp Ile	Phe Ala Gln Gln Arg Glu	180
170	175	
Ser Lys Glu Thr Ala Pro Gly Gly Thr	Glu Ser Gln Ser Leu Arg	195
185	190	
Thr Asn Glu Asn Lys Tyr Gln Gly Arg	Asp Asp Glu Ala Ser Asn	210
200	205	
Leu Val Gly Glu Glu Lys Leu Ile Pro	Pro Glu Glu Thr Pro Ala	225
215	220	
Pro Glu Thr Asp Ile Asn Leu Glu Val	Ser Phe Ala Glu Gln Ala	240
230	235	
Leu Asn Gln Lys Glu Arg Ser Lys Glu	Lys Ile Gln Lys Ser Lys	255
245	250	
Gly Asp Asp Ala Thr Leu Pro Ser Phe	Arg Leu Pro Lys Asp Lys	270
260	265	
Thr Gly Thr Thr Arg Ile Gly Asp Leu	Ala Pro Gln Asp Met Lys	285
275	280	
Lys Val Cys His Leu Ala Leu Ile Glu	Leu Thr Ala Leu Tyr Asp	300
290	295	
Val Leu Gly Ile Glu Leu Lys Gln Gln	Lys Ala Val Lys Ile Lys	315
305	310	
Thr Lys Asp Ser Gly Leu Phe Cys Val	Pro Leu Thr Ala Leu Leu	330
320	325	
Glu Gln Asp Gln Arg Lys Val Pro Gly	Met Arg Ile Pro Leu Ile	345
335	340	
Phe Gln Lys Leu Ile Ser Arg Ile Glu	Glu Arg Gly Leu Glu Thr	360
350	355	
Glu Gly Leu Leu Arg Ile Pro Gly Ala	Ala Ile Arg Ile Lys Asn	375
365	370	
Leu Cys Gln Glu Leu Glu Ala Lys Phe	Tyr Glu Gly Thr Phe Asn	390
380	385	
Trp Glu Ser Val Lys Gln His Asp Ala	Ala Ser Leu Leu Lys Leu	405
395	400	

Phe Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu	410	415	420
Lys Ala Phe Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln	425	430	435
Leu Gln Ala Leu Asn Leu Leu Val Ile Leu Leu Pro Asp Ala Asn	440	445	450
Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln Arg Val Ile	455	460	465
Asp Asn Lys Glu Lys Asn Lys Met Thr Val Met Asn Val Ala Met	470	475	480
Val Met Ala Pro Asn Leu Phe Met Cys His Ala Leu Gly Leu Lys	485	490	495
Ser Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala Asn	500	505	510
Thr Met His Leu Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile	515	520	525
Pro Lys Phe Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn	530	535	540
His Lys Lys Asp Lys Arg Ala Met Lys Lys Leu Leu Lys Lys Met	545	550	555
Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp Lys Ser Thr Asn	560	565	570
Asp Ala Asp Val Pro Gln Gly Val Ile Arg Val Gln Ala Pro His	575	580	585
Leu Ser Lys Val Ser Met Ala Ile Gln Leu Thr Glu Glu Leu Lys	590	595	600
Ala Ser Asp Val Leu Ala Arg Phe Leu Ser Gln Glu Ser Gly Val	605	610	615
Ala Gln Thr Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly	620	625	630
Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met Lys	635	640	645
Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val Ile Lys Ser	650	655	660

Lys Pro Leu

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 <111> 1327
 <112> DNA
 <113> Homo sapiens
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<221> unsure
 <222> 74, 1306
 <223> unknown base

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 gacccagggc cccggcactg cctngtgtga ggggctggca gctttccaac 100
 tgcagcaagt ggaggccccc gccagcttcg ggctgtggg caggggctca 150
 ggggggcagg ggtatggctg ccccgcccg caagcctgca cctgtctct 200
 cttgtgacc agtaacgcaa ggggatcacc tggggtccc tctgcagga 250

cctgtgtgag ctgcac atg gtg gag tgg agg acc tgc ctc 290
 Met Val Glu Trp Arg Thr Cys Leu
 1 5

tgg gtg gcc ccg ggc cag cag gtg tac agc ggg ctc tgg 329
 Ser Val Ala Pro Gly Gln Gln Val Tyr Ser Gly Leu Trp
 10 15 20

cgg gac aag gat gta acc atc aag tgt ggc att gag gag 368
 Arg Asp Lys Asp Val Thr Ile Lys Cys Gly Ile Glu Glu
 25 30

acc ctc gac tcc aag gcc cgg tgc gat gcg gcc ccc cgg 407
 Thr Leu Asp Ser Lys Ala Arg Ser Asp Ala Ala Pro Arg
 35 40 45

cgg gag ctg gta ctg ttt gac aag ccc acc cgg ggc acc 446
 Arg Glu Leu Val Leu Phe Asp Lys Pro Thr Arg Gly Thr
 50 55 60

tcc atc aag gaa ttc cgg gag atg acc ctc ggc ttc ctc 485
 Ser Ile Lys Glu Phe Arg Glu Met Thr Leu Gly Phe Leu
 65 70

aag gcg aac ctg gga gac ctg cct tcc ctg ccg gcg ctg 524
 Lys Ala Asn Leu Gly Asp Leu Pro Ser Leu Pro Ala Leu
 75 80 85

gtt ggc cag gtc ctg ctc atg gct gac ttc aac aag gac 563
 Val Gly Gln Val Leu Leu Met Ala Asp Phe Asn Lys Asp
 90 95

aac cgg gtc tcc ctg gcg gaa gcc aag tcc gtg tgg gcc 602
 Asn Arg Val Ser Leu Ala Glu Ala Lys Ser Val Trp Ala
 100 105 110

ctg ctg cag cgt aac caa ttc ctg ctg ctg ctg tcc ctg 641
 Leu Leu Gln Arg Asn Glu Phe Leu Leu Leu Leu Ser Leu
 115 120 125

cag gag aag gag cac gcc tcc aga ctg ctg ggc tac tgt 680
 Glu Glu Lys Glu His Ala Ser Arg Leu Leu Gly Tyr Cys
 130 135

ggg gac ctc tac ctc acc gag gcc gtg ccg cat gcc gcc 719
 Gly Asp Leu Tyr Leu Thr Glu Gly Val Pro His Gly Ala

140

145

150

tgg cac gcg gcc gcc ctc cca ccc ctg ttg cgc cca ctg 758
 Trp His Ala Ala Ala Leu Pro Pro Leu Leu Arg Pro Leu
 155 160

ctg ccg cct gcc ctg cag ggt gct ctc cag cag tgg ctg 797
 Leu Pro Pro Ala Leu Gln Gly Ala Leu Gln Gln Trp Leu
 165 170 175

ggg cct gcg tgg cct tgg cgg gcc aag atc gcc atc ggc 836
 Gly Pro Ala Trp Pro Trp Arg Ala Lys Ile Ala Ile Gly
 180 185 190

ctg ctg gag ttc gtg gag gag ctc ttc cac ggc tct tac 875
 Leu Leu Glu Phe Val Glu Glu Leu Phe His Gly Ser Tyr
 195 200

ggg act ttc tac atg tgt gag acc aca ctg gcc aac gtg 914
 Gly Thr Phe Tyr Met Cys Glu Thr Thr Leu Ala Asn Val
 205 210 215

ggc tac aca gcc acc tac gac ttc aag atg gcc gac ctg 953
 Gly Tyr Thr Ala Thr Tyr Asp Phe Lys Met Ala Asp Leu
 220 225

cag cag gtg gca ccc gag gcc acc gtg cgc cgc ttc ctg 992
 Gln Gln Val Ala Pro Glu Ala Thr Val Arg Arg Phe Leu
 230 235 240

cag ggc cgc cgc tgc gag cac agc acc gac tgc acc tac 1031
 Gln Gly Arg Arg Cys Glu His Ser Thr Asp Cys Thr Tyr
 245 250 255

ggg cgc gac tgc agg gcc ccg tgt gac agg ctc atg agg 1070
 Gly Arg Asp Cys Arg Ala Pro Cys Asp Arg Leu Met Arg
 260 265

cag tgc aag ggc gac ctc atc cag ccc aac ctg gcc aag 1109
 Gln Cys Lys Gly Asp Leu Ile Gln Pro Asn Leu Ala Lys
 270 275 280

gtg tgc gca ctg cta cgg ggc tac ctg ctg cct ggc gcg 1148
 Val Cys Ala Leu Leu Arg Gly Tyr Leu Leu Pro Gly Ala
 285 290

ccc gcc gac ctc cgc gag gag ctg ggc aca cag ctg cgc 1187
 Pro Ala Asp Leu Arg Glu Glu Leu Gly Thr Gln Leu Arg
 295 300 305

acc tgt acc acg ctg agc ggg ctg gcc agc cag gtg gag 1226
 Thr Cys Thr Thr Leu Ser Gly Leu Ala Ser Gln Val Glu
 310 315 320

gcc cat cac tgg ctg gtg ctc agc cac ctc aag act ctg 1265
 Ala His His Ser Leu Val Leu Ser His Leu Lys Thr Leu
 325 330

ctc tgg aag aag atc tcc aac acc aag tac tct t g 1300
 Leu Trp Lys Lys Ile Ser Asn Thr Lys Tyr Ser
 335 340 344

atgggnaatg agggettgcacaccttct 1327

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<211> 344

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 104

<223> unknown amino acid

<400> 16

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				20					25					30	
Gly	Ile	Glu	Glu	Thr	Leu	Asp	Ser	Lys	Ala	Arg	Ser	Asp	Ala	Ala	
				35					40					45	
Pro	Arg	Arg	Glu	Leu	Val	Leu	Phe	Asp	Lys	Pro	Thr	Arg	Gly	Thr	
				50					55					60	
Ser	Ile	Lys	Glu	Phe	Arg	Glu	Met	Thr	Leu	Gly	Phe	Leu	Lys	Ala	
				65					70					75	
Asn	Leu	Gly	Asp	Leu	Pro	Ser	Leu	Pro	Ala	Leu	Val	Gly	Gln	Val	
				80					85					90	
Leu	Leu	Met	Ala	Asp	Phe	Asn	Lys	Asp	Asn	Arg	Val	Ser	Xaa	Ala	
				95					100					105	
Glu	Ala	Lys	Ser	Val	Trp	Ala	Leu	Leu	Gln	Arg	Asn	Glu	Phe	Leu	
				110					115					120	
Leu	Leu	Leu	Ser	Leu	Gln	Glu	Lys	Glu	His	Ala	Ser	Arg	Leu	Leu	
				125					130					135	
Gly	Tyr	Cys	Gly	Asp	Leu	Tyr	Leu	Thr	Glu	Gly	Val	Pro	His	Gly	
				140					145					150	
Ala	Trp	His	Ala	Ala	Ala	Leu	Pro	Pro	Leu	Leu	Arg	Pro	Leu	Leu	
				155					160					165	
Pro	Pro	Ala	Leu	Gln	Gly	Ala	Leu	Gln	Gln	Trp	Leu	Gly	Pro	Ala	
				170					175					180	
Trp	Pro	Trp	Arg	Ala	Lys	Ile	Ala	Ile	Gly	Leu	Leu	Glu	Phe	Val	
				185					190					195	
Glu	Glu	Leu	Phe	His	Gly	Ser	Tyr	Gly	Thr	Phe	Tyr	Met	Cys	Glu	
				200					205					210	
Thr	Thr	Leu	Ala	Asn	Val	Gly	Tyr	Thr	Ala	Thr	Tyr	Asp	Phe	Lys	
				215					220					225	
Met	Ala	Asp	Leu	Gln	Gln	Val	Ala	Pro	Glu	Ala	Thr	Val	Arg	Arg	
				230					235					240	

Phe Leu Gln Gly Arg Arg Cys Glu His Ser Thr Asp Cys Thr Tyr
 245 250 255
 Gly Arg Asp Cys Arg Ala Pro Cys Asp Arg Leu Met Arg Gln Cys
 260 265 270
 Lys Gly Asp Leu Ile Gln Pro Asn Leu Ala Lys Val Cys Ala Leu
 275 280 285
 Leu Arg Gly Tyr Leu Leu Pro Gly Ala Pro Ala Asp Leu Arg Glu
 290 295 300
 Glu Leu Gly Thr Gln Leu Arg Thr Cys Thr Thr Leu Ser Gly Leu
 305 310 315
 Ala Ser Gln Val Glu Ala His His Ser Leu Val Leu Ser His Leu
 320 325 330
 Lys Thr Leu Leu Trp Lys Lys Ile Ser Asn Thr Lys Tyr Ser
 335 340

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 <112> DNA
 <113> Homo sapiens

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 1924, 1939, 1953, 1982, 1991-1992, 2000, 2443
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 tgctctngng cncggcaant cnggggagct actgcaccag gggcgctacc 150
 gggagccctg gcgcccctg cgaggncctgc gagcagaacc cagtgaactg 200
 attgtaaaaa ttacagagc ggaatcatat gctggtctcc aagagtttaa 250

agcagcctta gaagatttaa atg cag ttc ttt ttc aac ttc 291
 Met Gln Phe Phe Phe Asn Phe
 1 5

caa gat tgg cct gaa ggt cta ctt cag gaa ang gaa aaa 330
 Gln Asp Trp Pro Glu Gly Leu Leu Gln Glu Xaa Glu Lys
 10 15 20

gta ctc tgc gat gct ggt ttt tta ggt gat gcc tta caa 369
 Val Leu Cys Asp Ala Gly Phe Leu Gly Asp Ala Leu Gln
 25 30

ctc ttt ctt cag tgc tta gcc ctt gat gaa gat ttt gca 408
 Leu Phe Leu Gln Cys Leu Ala Leu Asp Glu Asp Phe Ala
 35 40 45

cct gca aag ctg caa gta caa aag att tta tgt gat tta 447

Pro Ala Lys Leu Gln Val Gln Lys Ile Leu Cys Asp Leu
50 55

tta tta cct gaa aac tta aaa gaa ggc ctg aag gaa tct 486
Leu Leu Pro Glu Asn Leu Lys Glu Gly Leu Lys Glu Ser
60 65 70

tcc tgg agt tca tta cca tgt act aaa aac aga cct ttt 525
Ser Trp Ser Ser Leu Pro Cys Thr Lys Asn Arg Pro Phe
75 80 85

gat ttt cat tca gtg atg gaa gag tct cag tct ctc aat 564
Asp Phe His Ser Val Met Glu Glu Ser Gln Ser Leu Asn
90 95

gaa cct agc cca aag cag agt gaa gaa ata cca gag gtc 603
Glu Pro Ser Pro Lys Gln Ser Glu Glu Ile Pro Glu Val
100 105 110

act tca gag cct gtc aaa gga agc tta aac cgt gct cag 642
Thr Ser Glu Pro Val Lys Gly Ser Leu Asn Arg Ala Gln
115 120

tca gca cag tct ata aat tca aca gaa atg cct gcc aga 681
Ser Ala Gln Ser Ile Asn Ser Thr Glu Met Pro Ala Arg
125 130 135

gag gac tgt tta aaa aaa gtg tcc tca gaa cct gtt ctg 720
Glu Asp Cys Leu Lys Lys Val Ser Ser Glu Pro Val Leu
140 145 150

tca gtt caa gaa aaa ggt gtt ctg ctg aaa aga aag ttg 759
Ser Val Gln Glu Lys Gly Val Leu Leu Lys Arg Lys Leu
155 160

tct ctt tta gaa cag gat gtg att gta aat gaa gat gga 798
Ser Leu Leu Glu Gln Asp Val Ile Val Asn Glu Asp Gly
165 170 175

aga aat aag ctg aaa aaa caa gga gaa act ccc aat gaa 837
Arg Asn Lys Leu Lys Lys Gln Gly Glu Thr Pro Asn Glu
180 185

gtc tgt atg ttt tcc tta gct tat ggt gat att cca gaa 876
Val Cys Met Phe Ser Leu Ala Tyr Gly Asp Ile Pro Glu
190 195 200

gaa tta atc gat gtc tca gat ttc gag tgt tct ctc tgc 915
Glu Leu Ile Asp Val Ser Asp Phe Glu Cys Ser Leu Cys
205 210 215

atg agg ttg ttt ttt gag cca gta aca acc cct tgc qqa 954
Met Arg Leu Phe Phe Glu Pro Val Thr Thr Pro Cys Gly
220 225

cat tgg ttc tgt aag aat tgt ctt gag cgt tgt tta gat 993
His Ser Phe Cys Lys Asn Cys Leu Glu Arg Cys Leu Asp
230 235 240

cat gca cca tat tgt cct ctt tgc aaa gaa agc tta aat 1032
His Ala Pro Tyr Cys Pro Leu Cys Lys Glu Ser Leu Asn

gag tat cta gca gat agg agg tac tct gtc aca cag ctg 1071
 Glu Tyr Leu Ala Asp Arg Arg Tyr Cys Val Thr Gln Leu
 255 260 265

ttg gaa gaa tta ata gtg aag tat ctg cct gat gaa ctg 1110
 Leu Glu Glu Leu Ile Val Lys Tyr Leu Pro Asp Glu Leu
 270 275 280

tct gag aca aaa aaa ata tat gaa gaa gaa act cct gaa 1149
 Ser Glu Arg Lys Lys Ile Tyr Glu Glu Glu Thr Ala Glu
 285 290

ctc tca cac ttg acc aag aat gtt cca ata ttt gtt tgc 1188
 Leu Ser His Leu Thr Lys Asn Val Pro Ile Phe Val Cys
 295 300 305

act atg gcc tac ccc act gtg cct tgc cct ctc cat gta 1227
 Thr Met Ala Tyr Pro Thr Val Pro Cys Pro Leu His Val
 310 315

ttt gag cca aga tac aga ttg atg att cga aga agt ata 1265
 Phe Glu Pro Arg Tyr Arg Leu Met Ile Arg Arg Ser Ile
 320 325 330

cag act gga acc aaa cag ttt ggc atg tgt gtc agt gat 1305
 Gln Thr Gly Thr Lys Gln Phe Gly Met Cys Val Ser Asp
 335 340 345

aca caa aat agt ttt gca gat tat ggt tgt atg tta caa 1344
 Thr Gln Asn Ser Phe Ala Asp Tyr Gly Cys Met Leu Gln
 350 355

att aga aac gtg cat ttc tta ccg gac gga agg tct gtg 1383
 Ile Arg Asn Val His Phe Leu Pro Asp Gly Arg Ser Val
 360 365 370

gtt gat aca gtt gga gga aag cgg ttt agg gtt tta aaa 1422
 Val Asp Thr Val Gly Gly Lys Arg Phe Arg Val Leu Lys
 375 380

aga gga atg aaa gat gga tat tgc act gcc gac att gaa 1461
 Arg Gly Met Lys Asp Gly Tyr Cys Thr Ala Asp Ile Glu
 385 390 395

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 Tyr Leu Glu Asp Val Lys Val Glu Asn Glu Asp Glu Ile
 400 405 410

aag aat ctc aga gag ctt cat gat ttg gtt tac tct caa 1539
 Lys Asn Leu Arg Glu Leu His Asp Leu Val Tyr Ser Gln
 415 420

gcc tgc agc tgg ttt bag aat tta aga gac aga ttt cga 1578
 Ala Cys Ser Trp Phe Gln Asn Leu Arg Asp Arg Phe Arg
 425 430 435

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 Ser Gln Ile Leu Gln His Phe Gly Ser Met Pro Glu Xaa
 440 445

gag gaa aac ctt cag gca gcc cct aat gga cct gca tgg 1656
 Glu Glu Asn Leu Gln Ala Ala Pro Asn Gly Pro Ala Trp
 450 455 460

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 Cys Trp Trp Leu Leu Ala Val Leu Pro Val Asp Pro Arg
 465 470 475

tac cag ctg tgg gtt ttg tca atg aag tct ttg aaa gaa 1734
 Tyr Gln Leu Ser Val Leu Ser Met Lys Ser Leu Lys Glu
 480 485

cgg ttg acc aag ata cag cat ata ctg acc tat ttt tct 1773
 Arg Leu Thr Lys Ile Gln His Ile Leu Thr Tyr Phe Ser
 490 495 500

aga gac caa tct aag t a actaactctt tggatctccc 1810
 Arg Asp Gln Ser Lys
 505 506

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 Ala Leu Gln Leu Phe Leu Gln Cys Leu Ala Leu Asp Glu Asp Phe
 35 40 45
 Ala Pro Ala Lys Leu Gln Val Gln Lys Ile Leu Cys Asp Leu Leu
 50 55 60
 Leu Pro Glu Asn Leu Lys Glu Gly Leu Lys Glu Ser Ser Trp Ser
 65 70 75
 Ser Leu Pro Cys Thr Lys Asn Arg Pro Phe Asp Phe His Ser Val
 80 85 90
 Met Glu Glu Ser Gln Ser Leu Asn Glu Pro Ser Pro Lys Gln Ser
 95 100 105
 Glu Glu Ile Pro Glu Val Thr Ser Glu Pro Val Lys Gly Ser Leu
 110 115 120
 Asn Arg Ala Gln Ser Ala Gln Ser Ile Asn Ser Thr Glu Met Pro
 125 130 135
 Ala Arg Glu Asp Cys Leu Lys Lys Val Ser Ser Glu Pro Val Leu
 140 145 150
 Ser Val Gln Glu Lys Gly Val Leu Leu Lys Arg Lys Leu Ser Leu
 155 160 165
 Leu Glu Gln Asp Val Ile Val Asn Glu Asp Gly Arg Asn Lys Leu
 170 175 180
 Lys Lys Gln Gly Glu Thr Pro Asn Glu Val Cys Met Phe Ser Leu
 185 190 195
 Ala Tyr Gly Asp Ile Pro Glu Glu Leu Ile Asp Val Ser Asp Phe

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Glu Cys Ser Leu Cys Met Arg Leu Phe Phe Glu Pro Val Thr Thr 215	220	225
Pro Cys Gly His Ser Phe Cys Lys Asn Cys Leu Glu Arg Cys Leu 230	235	240
Asp His Ala Pro Tyr Cys Pro Leu Cys Lys Glu Ser Leu Asn Glu 245	250	255
Tyr Leu Ala Asp Arg Arg Tyr Cys Val Thr Gln Leu Leu Glu Glu 260	265	270
Leu Ile Val Lys Tyr Leu Pro Asp Glu Leu Ser Glu Arg Lys Lys 275	280	285
Ile Tyr Glu Glu Glu Thr Ala Glu Leu Ser His Leu Thr Lys Asn 290	295	300
Val Pro Ile Phe Val Cys Thr Met Ala Tyr Pro Thr Val Pro Cys 305	310	315
Pro Leu His Val Phe Glu Pro Arg Tyr Arg Leu Met Ile Arg Arg 320	325	330
Ser Ile Gln Thr Gly Thr Lys Gln Phe Gly Met Cys Val Ser Asp 335	340	345
Thr Gln Asn Ser Phe Ala Asp Tyr Gly Cys Met Leu Gln Ile Arg 350	355	360
Asn Val His Phe Leu Pro Asp Gly Arg Ser Val Val Asp Thr Val 365	370	375
Gly Gly Lys Arg Phe Arg Val Leu Lys Arg Gly Met Lys Asp Gly 380	385	390
Tyr Cys Thr Ala Asp Ile Glu Tyr Leu Glu Asp Val Lys Val Glu 395	400	405
Asn Glu Asp Glu Ile Lys Asn Leu Arg Glu Leu His Asp Leu Val 410	415	420
Tyr Ser Gln Ala Cys Ser Trp Phe Gln Asn Leu Arg Asp Arg Phe 425	430	435
Arg Ser Gln Ile Leu Gln His Phe Gly Ser Met Pro Xaa Arg Glu 440	445	450
Glu Asn Leu Gln Ala Ala Pro Asn Gly Pro Ala Trp Cys Trp Trp 455	460	465
Leu Leu Ala Val Leu Pro Val Asp Pro Arg Tyr Gln Leu Ser Val 470	475	480
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tcagtgtgga gtatctcaaa gcctttcagg ctgtccagaa ttttccaacc 200
aagaagcagc aactacaggg cttttgaacc ctttctttta ctcattcctg 250
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accccccccc 310

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ccagaatctt ccaaccaaga agcagc 26

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tgc 53

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cagtcacaaa tttgcaacaa ataattacaa aagtttctaq ggcagcatga 150
atataaacca tgttgcaqca tgggtgatcta actgtgatat gaataaggca 200
taactaacat ttgcaccgag accagaatta aaaacaaaaa caaactttaa 250
aagcttagtt ctatattaaa cttcttctct tttccagat ccttaatggg 300
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attacacaaa tgggcagtta atgtgaaaag ccccttaaaa tgtacaaact 400
aactgggtact gaattgagtt ctccctttac ctttatgtac aattaaatgt 450
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cctggccaac cagcgccggc agggaaaggca ggtctcccag gttcgccttg 150
aggaagccga gggtcatttc ccggaattcc ttgatggagg tgccccgggt 200
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ctagagacca atctaagtaa 20

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<400> 29
ctccaacacc aagtactctt ga 22

09/684,458

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PRO-C-MG.12	SEQ ID 3	SEQ ID 4
PRO-C-MG.45	SEQ ID 17	SEQ ID 18
PRO-C-MG.64	SEQ ID 15	SEQ ID 16
PRO-C-MG.72	SEQ ID 13	SEQ ID 14

3/11/15